

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Anderson, Dirk M.  
Galibert, Laurent  
Maraskovsky, Eugene
- (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Immunex Corporation, Law Department
  - (B) STREET: 51 University Street
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: Apple Power Macintosh
  - (C) OPERATING SYSTEM: Apple Operating System 7.5.5
  - (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 22 DECEMBER 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: USSN 60/064,671
  - (B) FILING DATE: 14 OCTOBER 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: USSN 08/813,509
  - (B) FILING DATE: 07 MARCH 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: USSN 08/772,330 (60/064,671)
  - (B) FILING DATE: 23 DECEMBER 1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Perkins, Patricia Anne
  - (B) REGISTRATION NUMBER: 34,693
  - (C) REFERENCE/DOCKET NUMBER: 2852-A
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206)587-0430
  - (B) TELEFAX: (206)233-0644

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3115 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: HOMO SAPIENS

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS  
(B) CLONE: 9D-8A

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 93..1868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG	60
GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT	113
Val Ala Leu Gln Ile Ala Pro	
1 5	
CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC	161
Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn	
10 15 20	
AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT	209
Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser	
25 30 35	
GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG	257
Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp	
40 45 50 55	
AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG	305
Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys	
60 65 70	
GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC	353
Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys	
75 80 85	
GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC	401
Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg	
90 95 100	
CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG	449
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln	
105 110 115	
CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT	497
Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser	
120 125 130 135	
GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC	545
Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr	
140 145 150	
TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG	593
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala	
155 160 165	
GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT	641
Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His	
170 175 180	
GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC	689
Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala	
185 190 195	

CTG Leu 200	GTG Val	GCT Ala	GCC Ala	ATC Ile	ATC Ile 205	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 210	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 215	737
GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 220	TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 225	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 230	CGC Arg	785
CTA Leu	AGT Ser	GGA Gly	GAT Asp 235	AAG Lys	GAG Glu	TCC Ser	TCA Ser	GGT Gly 240	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 245	ACA Thr	CAC His	833
ACG Thr	GCA Ala	AAC Asn 250	TTT Phe	GGT Gly	CAG Gln	CAG Gln	GGA Gly 255	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 260	TTA Leu	CTG Leu	CTG Leu	881
ACT Thr	CTG Leu 265	GAG Glu	GAG Glu	AAG Lys	ACA Thr	TTT Phe 270	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 275	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	929
GGT Gly 280	GGT Gly	GTC Val	TGT Cys	CAG Gln	GGC Gly 285	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 290	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 295	977
GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 300	ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 305	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 310	GAG Glu	1025
GAA Glu	GAC Asp	AGC Ser	TTC Phe 315	AGA Arg	CAG Gln	ATG Met	CCC Pro	ACA Thr 320	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG Met 325	GAC Asp	AGG Arg	1073
CCC Pro	TCC Ser	CAG Gln 330	CCC Pro	ACA Thr	GAC Asp	CAG Gln	TTA Leu 335	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG Glu 340	CCT Pro	GGA Gly	AGC Ser	1121
AAA Lys	TCC Ser 345	ACA Thr	CCT Pro	CCT Pro	TTC Phe	TCT Ser 350	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 355	GGG Gly	GAG Glu	AAT Asn	GAC Asp	1169
AGT Ser 360	TTA Leu	AGC Ser	CAG Gln	TGC Cys	TTC Phe 365	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 370	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu 375	1217
AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 380	GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 385	ACT Thr	GAT Asp	TGG Trp	ACT Thr 390	CCC Pro	ATG Met	1265
TCC Ser	TCT Ser	GAA Glu 395	AAC Asn	TAC Tyr	TTG Leu	CAA Gln	AAA Lys	GAG Glu 400	GTG Val	GAC Asp	AGT Ser	GGC Gly 405	CAT His 405	TGC Cys	CCG Pro	1313
CAC His	TGG Trp 410	GCA Ala	GCC Ala	AGC Ser	CCC Pro	AGC Ser	CCC Pro 415	AAC Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 420	TGC Cys	ACA Thr	GGC Gly	1361
TGC Cys 425	CGG Arg	AAC Asn	CCT Pro	CCT Pro	GGG Gly 430	GAG Glu	GAC Asp	TGT Cys	GAA Glu	CCC Pro 435	CTC Leu	GTG Val	GGT Gly	TCC Ser	CCA Pro	1409
AAA Lys 440	CGT Arg	GGA Gly	CCC Pro	TTG Leu	CCC Pro 445	CAG Gln	TGC Cys	GCC Ala	TAT Tyr	GGC Gly 450	ATG Met	GGC Gly	CTT Leu	CCC Pro	CCT Pro 455	1457
GAA Glu	GAA Glu	GAA Glu	GCC Ala	AGC Ser 460	AGG Arg	ACG Thr	GAG Glu	GCC Ala	AGA Arg 465	GAC Asp	CAG Gln	CCC Pro	GAG Glu	GAT Asp 470	GGG Gly	1505

GCT Ala	GAT Asp	GGG Gly	AGG Arg 475	CTC Leu	CCA Pro	AGC Ser	TCA Ser	GCG Ala 480	AGG Arg	GCA Ala	GGT Gly	GCC Ala	GGG Gly 485	TCT Ser	GGA Gly	1553		
AGC Ser	TCC Ser	CCT Pro 490	GGT Gly	GGC Gly	CAG Gln	TCC Ser	CCT Pro 495	GCA Ala	TCT Ser	GGA Gly	AAT Asn	GTG Val 500	ACT Thr	GGA Gly	AAC Asn	1601		
AGT Ser	AAC Asn 505	TCC Ser	ACG Thr	TTC Phe	ATC Ile	TCC Ser 510	AGC Ser	GGG Gly	CAG Gln	GTG Val	ATG Met 515	AAC Asn	TTC Phe	AAG Lys	GGC Gly	1649		
GAC Asp 520	ATC Ile	ATC Ile	GTG Val	GTC Val	TAC Tyr 525	GTC Val	AGC Ser	CAG Gln	ACC Thr	TCG Ser 530	CAG Gln	GAG Glu	GGC Gly	GCG Ala	GCG Ala 535	1697		
GCG Ala	GCT Ala	GCG Ala	GAG Glu	CCC Pro 540	ATG Met	GGC Gly	CGC Arg	CCG Pro	GTG Val 545	CAG Gln	GAG Glu	GAG Glu	ACC Thr	CTG Leu 550	GCG Ala	1745		
CGC Arg	CGA Arg	GAC Asp 555	TCC Ser	TTC Phe	GCG Ala	GGG Gly	AAC Asn	GGC Gly 560	CCG Pro	CGC Arg	TTC Phe	CCG Pro	GAC Asp 565	CCG Pro	TGC Cys	1793		
GGC Gly	GGC Gly	CCC Pro 570	GAG Glu	GGG Gly	CTG Leu	CGG Arg	GAG Glu 575	CCG Pro	GAG Glu	AAG Lys	GCC Ala 580	TCG Ser	AGG Arg	CCG Pro	GTG Val	1841		
CAG Gln 585	GAG Glu	CAA Gln	GGC Gly	GGG Gly	GCC Ala	AAG Lys 590	GCT Ala	TGA	GCGCCCCCA TGGCTGGGAG							1888		
CCCGAAGCTC			GGAGCCAGGG			CTCGCGAGGG			CAGCACCGCA			GCCTCTGCCC			CAGCCCCGGC			1948
CACCCAGGGA			TCGATCGGTA			CAGTCGAGGA			AGACCACCCG			GCATTCTCTG			CCCACTTTGC			2008
CTTCCAGGAA			ATGGGCTTTT			CAGGAAGTGA			ATTGATGAGG			ACTGTCCCCA			TGCCACGGA			2068
TGCTCAGCAG			CCCGCCGCAC			TGGGGCAGAT			GTCTCCCCTG			CCACTCCTCA			AACTCGCAGC			2128
AGTAATTTGT			GGCACTATGA			CAGCTATTTT			TATGACTATC			CTGTTCTGTG			GGGGGGGGGT			2188
CTATGTTTTT			CCCCCATATT			TGTATTCCTT			TTCATAACTT			TTCTTGATAT			CTTTCCTCCC			2248
TCTTTTTTAA			TGTAAGGTT			TTCTCAAAA			TTCTCCTAAA			GGTGAGGGTC			TCTTTCTTTT			2308
CTCTTTTCCT			TTTTTTTTTTC			TTTTTTTGGC			AACCTGGCTC			TGGCCCAGGC			TAGAGTGCAG			2368
TGGTGCGATT			ATAGCCCGGT			GCAGCCTCTA			ACTCCTGGGC			TCAAGCAATC			CAAGTGATCC			2428
TCCCACCTCA			ACCTTCGGAG			TAGCTGGGAT			CACAGCTGCA			GGCCACGCCC			AGCTTCCTCC			2488
CCCCGACTCC			CCCCCCCCCAG			AGACACGGTC			CCACCATGTT			ACCCAGCCTG			GTCTCAAACT			2548
CCCCAGCTAA			AGCAGTCCTC			CAGCCTCGGC			CTCCCAAAGT			ACTGGGATTA			CAGGCGTGAG			2608
CCCCCACGCT			GGCCTGCTTT			ACGTATTTTC			TTTTGTGCCC			CTGCTCACAG			TGTTTTAGAG			2668
ATGGCTTTCC			CAGTGTGTGT			TCATTGTAAA			CACTTTTGGG			AAAGGGCTAA			ACATGTGAGG			2728
CCTGGAGATA			GTTGCTAAGT			TGCTAGGAAC			ATGTGGTGGG			ACTTTCATAT			TCTGAAAAAT			2788
GTTCTATATT			CTCATTTTTT			TAAAAGAAAG			AAAAAAGGAA			ACCCGATTTA			TTTCTCCTGA			2848
ATCTTTTTTAA			GTTTGTGTGCG			TTCCTTAAGC			AGAACTAAGC			TCAGTATGTG			ACCTTACCCG			2908
CTAGGTGGTT			AATTTATCCA			TGCTGGCAGA			GGCACTCAGG			TACTTGGTAA			GCAAATTTCT			2968
AAAACTCCAA			GTTGCTGCAG			CTTGGCATTC			TTCTTATTCT			AGAGGTCTCT			CTGGAAAAGA			3028

TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA 3088  
 GAATAAAGTT GAAATTTTAA AAAAAAA 3115

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu  
 1 5 10 15  
 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser  
 20 25 30  
 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro  
 35 40 45  
 Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His  
 50 55 60  
 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn  
 65 70 75 80  
 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser  
 85 90 95  
 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu  
 100 105 110  
 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro  
 115 120 125  
 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys  
 130 135 140  
 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His  
 145 150 155 160  
 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg  
 165 170 175  
 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu  
 180 185 190  
 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val  
 195 200 205  
 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp  
 210 215 220  
 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly  
 225 230 235 240  
 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala  
 245 250 255  
 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu  
 260 265 270  
 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val  
 275 280 285

Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu  
 290 295 300  
 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr  
 305 310 315 320  
 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu  
 325 330 335  
 Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro  
 340 345 350  
 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr  
 355 360 365  
 Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys  
 370 375 380  
 Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu  
 385 390 395 400  
 Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn  
 405 410 415  
 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys  
 420 425 430  
 Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala  
 435 440 445  
 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala  
 450 455 460  
 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala  
 465 470 475 480  
 Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala  
 485 490 495  
 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly  
 500 505 510  
 Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln  
 515 520 525  
 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro  
 530 535 540  
 Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly  
 545 550 555 560  
 Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro  
 565 570 575  
 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS  
(B) CLONE: 9D-15C
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 39..1391

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC	53
Met Ala Pro Arg Ala	
1 5	
CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC	101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu	
10 15 20	
GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG	149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu	
25 30 35	
AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA	197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly	
40 45 50	
AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG	245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu	
55 60 65	
CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA	293
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys	
70 75 80 85	
TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG	341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val	
90 95 100	
GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG	389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly	
105 110 115	
TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC	437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys	
120 125 130	
GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA	485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr	
135 140 145	
GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC	533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser	
150 155 160 165	
ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA	581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg	
170 175 180	
GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT	629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser	
185 190 195	

CTG Leu	CCA Pro	GCT Ala 200	AGA Arg	AAA Lys	CCA Pro	CCA Pro	AAT Asn 205	GAA Glu	CCC Pro	CAT His	GTT Val	TAC Tyr 210	TTG Leu	CCC Pro	GGT Gly	677
TTA Leu	ATA Ile 215	ATT Ile	CTG Leu	CTT Leu	CTC Leu	TTC Phe 220	GCG Ala	TCT Ser	GTG Val	GCC Ala	CTG Leu 225	GTG Val	GCT Ala	GCC Ala	ATC Ile	725
ATC Ile 230	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 235	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 240	GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 245	773
TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 250	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 255	CGC Arg	CTA Leu	AGT Ser	GGA Gly	GAT Asp 260	AAG Lys	821
GAG Glu	TCC Ser	TCA Ser	GGT Gly 265	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 270	ACA Thr	CAC His	ACG Thr	GCA Ala	AAC Asn 275	TTT Phe	GGT Gly	869
CAG Gln	CAG Gln	GGA Gly 280	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 285	TTA Leu	CTG Leu	CTG Leu	ACT Thr	CTG Leu 290	GAG Glu	GAG Glu	AAG Lys	917
ACA Thr 295	TTT Phe	CCA Pro	GAA Glu	GAT Asp	ATG Met 300	TGC Cys	TAC Tyr	CCA Pro	GAT Asp	CAA Gln 305	GGT Gly	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
GGC Gly 310	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 315	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 320	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 325	1013
ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 330	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 335	GAG Glu	GAA Glu	GAC Asp	AGC Ser	TTC Phe 340	AGA Arg	1061
CAG Gln	ATG Met	CCC Pro	ACA Thr 345	GAA Glu	GAT Asp	GAA Glu	TAC Tyr 350	ATG Met	GAC Asp	AGG Arg	CCC Pro	TCC Ser	CAG Gln 355	CCC Pro	ACA Thr	1109
GAC Asp	CAG Gln 360	TTA Leu	CTG Phe	TTC Leu	CTC Leu	ACT Thr	GAG Glu 365	CCT Pro	GGA Gly	AGC Ser	AAA Lys	TCC Ser 370	ACA Thr	CCT Pro	CCT Pro	1157
TTC Phe 375	TCT Ser	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 380	GGG Gly	GAG Glu	AAT Asn	GAC Asp	AGT Ser 385	TTA Leu	AGC Ser	CAG Gln	TGC Cys	1205
TTC Phe 390	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 395	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu 400	AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 405	1253
GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 410	ACT Thr	GAT Asp	TGG Trp	ACT Thr	CCC Pro 415	ATG Met	TCC Ser	TCT Ser	GAA Glu 420	AAC Asn	TAC Tyr	1301
TTG Leu	CAA Gln	AAA Lys	GAG Glu 425	GTG Val	GAC Asp	AGT Ser	GGC Gly	CAT His 430	TGC Cys	CCG Pro	CAC His	TGG Trp	GCA Ala 435	GCC Ala	AGC Ser	1349
CCC Pro	AGC Ser	CCC Pro	AAC Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 445	TGC Cys	ACA Thr	GGC Gly	TGC Cys	CGG Arg 450	AAC Asn			1391

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids  
(B) TYPE: amino acid



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu  
 1 5 10 15  
 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro  
 20 25 30  
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn  
 35 40 45  
 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
 50 55 60  
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
 65 70 75 80  
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
 85 90 95  
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
 100 105 110  
 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
 115 120 125  
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
 130 135 140  
 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
 145 150 155 160  
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
 165 170 175  
 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
 180 185 190  
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
 195 200 205  
 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala  
 210 215 220  
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
 225 230 235 240  
 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg  
 245 250 255  
 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His  
 260 265 270  
 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu  
 275 280 285  
 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln  
 290 295 300  
 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln  
 305 310 315 320  
 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu  
 325 330 335

Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg  
 340 345 350  
 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser  
 355 360 365  
 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp  
 370 375 380  
 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu  
 385 390 395 400  
 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met  
 405 410 415  
 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro  
 420 425 430  
 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly  
 435 440 445  
 Cys Arg Asn  
 450

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3136 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
  - (B) CLONE: FULL LENGTH RANK
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 39..1886

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC	53
Met Ala Pro Arg Ala	
1 5	
CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC	101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu	
10 15 20	
GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG	149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu	
25 30 35	
AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA	197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly	
40 45 50	

AAG Lys	TAC Tyr 55	ATG Met	TCT Ser	TCT Ser	AAA Lys	TGC Cys 60	ACT Thr	ACT Thr	ACC Thr	TCT Ser	GAC Asp 65	AGT Ser	GTA Val	TGT Cys	CTG Leu	245
CCC Pro 70	TGT Cys	GGC Gly	CCG Pro	GAT Asp	GAA Glu 75	TAC Tyr	TTG Leu	GAT Asp	AGC Ser	TGG Trp 80	AAT Asn	GAA Glu	GAA Glu	GAT Asp	AAA Lys 85	293
TGC Cys	TTG Leu	CTG Leu	CAT His	AAA Lys 90	GTT Val	TGT Cys	GAT Asp	ACA Thr	GGC Gly 95	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 100	GTG Val	341
GTC Val	GCC Ala	GGC Gly	AAC Asn 105	AGC Ser	ACG Thr	ACC Thr	CCC Pro	CGG Arg 110	CGC Arg	TGC Cys	GCG Ala	TGC Cys	ACG Thr 115	GCT Ala	GGG Gly	389
TAC Tyr	CAC His	TGG Trp 120	AGC Ser	CAG Gln	GAC Asp	TGC Cys	GAG Glu 125	TGC Cys	TGC Cys	CGC Arg	CGC Arg	AAC Asn 130	ACC Thr	GAG Glu	TGC Cys	437
GCG Ala 135	CCG Pro	GGC Gly	CTG Leu	GGC Gly	GCC Ala	CAG Gln 140	CAC His	CCG Pro	TTG Leu	CAG Gln	CTC Leu 145	AAC Asn	AAG Lys	GAC Asp	ACA Thr	485
GTG Val 150	TGC Cys	AAA Lys	CCT Pro	TGC Cys	CTT Leu 155	GCA Ala	GGC Gly	TAC Tyr	TTC Phe	TCT Ser 160	GAT Asp	GCC Ala	TTT Phe	TCC Ser	TCC Ser 165	533
ACG Thr	GAC Asp	AAA Lys	TGC Cys	AGA Arg 170	CCC Pro	TGG Trp	ACC Thr	AAC Asn	TGT Cys 175	ACC Thr	TTC Phe	CTT Leu	GGA Gly	AAG Lys 180	AGA Arg	581
GTA Val	GAA Glu	CAT His	CAT His 185	GGG Gly	ACA Thr	GAG Glu	AAA Lys	TCC Ser 190	GAT Asp	GCG Ala	GTT Val	TGC Cys	AGT Ser 195	TCT Ser	TCT Ser	629
CTG Leu	CCA Pro	GCT Ala 200	AGA Arg	AAA Lys	CCA Pro	CCA Pro	AAT Asn 205	GAA Glu	CCC Pro	CAT His	GTT Val 210	TAC Tyr	TTG Leu	CCC Pro	GGT Gly	677
TTA Leu 215	ATA Ile	ATT Ile	CTG Leu	CTT Leu	CTC Leu	TTC Phe 220	GCG Ala	TCT Ser	GTG Val	GCC Ala	CTG Leu 225	GTG Val	GCT Ala	GCC Ala	ATC Ile	725
ATC Ile 230	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 235	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 240	GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 245	773
TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 250	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 255	CGC Arg	CTA Leu	AGT Ser	GGA Gly	GAT Asp 260	AAG Lys	821
GAG Glu	TCC Ser	TCA Ser	GGT Gly 265	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 270	ACA Thr	CAC His	ACG Thr	GCA Ala	AAC Asn 275	TTT Phe	GGT Gly	869
CAG Gln	CAG Gln	GGA Gly 280	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 285	TTA Leu	CTG Leu	CTG Leu	ACT Thr	CTG Leu 290	GAG Glu	GAG Glu	AAG Lys	917
ACA Thr 295	TTT Phe	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 300	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	GGT Gly 305	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
GGC Gly 310	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 315	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 320	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 325	1013

ATG	CTC	TCA	TTG	GTC	AGC	AAG	ACC	GAG	ATA	GAG	GAA	GAC	AGC	TTC	AGA	1061
Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	Glu	Asp	Ser	Phe	Arg	
				330					335					340		
CAG	ATG	CCC	ACA	GAA	GAT	GAA	TAC	ATG	GAC	AGG	CCC	TCC	CAG	CCC	ACA	1109
Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	Pro	Ser	Gln	Pro	Thr	
			345					350					355			
GAC	CAG	TTA	CTG	TTC	CTC	ACT	GAG	CCT	GGA	AGC	AAA	TCC	ACA	CCT	CCT	1157
Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	Lys	Ser	Thr	Pro	Pro	
		360					365					370				
TTC	TCT	GAA	CCC	CTG	GAG	GTG	GGG	GAG	AAT	GAC	AGT	TTA	AGC	CAG	TGC	1205
Phe	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	
	375					380					385					
TTC	ACG	GGG	ACA	CAG	AGC	ACA	GTG	GGT	TCA	GAA	AGC	TGC	AAC	TGC	ACT	1253
Phe	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	Ser	Cys	Asn	Cys	Thr	
390					395					400					405	
GAG	CCC	CTG	TGC	AGG	ACT	GAT	TGG	ACT	CCC	ATG	TCC	TCT	GAA	AAC	TAC	1301
Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	Ser	Ser	Glu	Asn	Tyr	
				410					415					420		
TTG	CAA	AAA	GAG	GTG	GAC	AGT	GGC	CAT	TGC	CCG	CAC	TGG	GCA	GCC	AGC	1349
Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	His	Trp	Ala	Ala	Ser	
			425					430					435			
CCC	AGC	CCC	AAC	TGG	GCA	GAT	GTC	TGC	ACA	GGC	TGC	CGG	AAC	CCT	CCT	1397
Pro	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	Cys	Arg	Asn	Pro	Pro	
		440					445					450				
GGG	GAG	GAC	TGT	GAA	CCC	CTC	GTG	GGT	TCC	CCA	AAA	CGT	GGA	CCC	TTG	1445
Gly	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	Lys	Arg	Gly	Pro	Leu	
	455					460					465					
CCC	CAG	TGC	GCC	TAT	GGC	ATG	GGC	CTT	CCC	CCT	GAA	GAA	GAA	GCC	AGC	1493
Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	Glu	Glu	Glu	Ala	Ser	
470					475					480					485	
AGG	ACG	GAG	GCC	AGA	GAC	CAG	CCC	GAG	GAT	GGG	GCT	GAT	GGG	AGG	CTC	1541
Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	Ala	Asp	Gly	Arg	Leu	
				490					495					500		
CCA	AGC	TCA	GCG	AGG	GCA	GGT	GCC	GGG	TCT	GGA	AGC	TCC	CCT	GGT	GGC	1589
Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	Ser	Ser	Pro	Gly	Gly	
			505					510					515			
CAG	TCC	CCT	GCA	TCT	GGA	AAT	GTG	ACT	GGA	AAC	AGT	AAC	TCC	ACG	TTC	1637
Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	
		520					525					530				
ATC	TCC	AGC	GGG	CAG	GTG	ATG	AAC	TTC	AAG	GGC	GAC	ATC	ATC	GTG	GTC	1685
Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	
	535					540					545					
TAC	GTC	AGC	CAG	ACC	TCG	CAG	GAG	GGC	GCG	GCG	GCG	GCT	GCG	GAG	CCC	1733
Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	Ala	Ala	Ala	Glu	Pro	
550					555					560					565	
ATG	GGC	CGC	CCG	GTG	CAG	GAG	GAG	ACC	CTG	GCG	CGC	CGA	GAC	TCC	TTC	1781
Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	Arg	Arg	Asp	Ser	Phe	
				570					575					580		
GCG	GGG	AAC	GGC	CCG	CGC	TTC	CCG	GAC	CCG	TGC	GGC	GGC	CCC	GAG	GGG	1829
Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys	Gly	Gly	Pro	Glu	Gly	
			585					590					595			

CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG CAG GAG CAA GGC GGG	1877
Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly	
600 605 610	
GCC AAG GCT TGAGCGCCCC CCATGGCTGG GAGCCCCGAAG CTCGGAGCCA	1926
Ala Lys Ala	
615	
GGGCTCGCGA GGGCAGCACC GCAGCCTCTG CCCCAGCCCC GGCCACCCAG GGATCGATCG	1986
GTACAGTCGA GGAAGACCAC CCGGCATTCT CTGCCCACTT TGCCTTCCAG GAAATGGGCT	2046
TTTCAGGAAG TGAATTGATG AGGACTGTCC CCATGCCAC GGTATGCTCAG CAGCCCCGCCG	2106
CACTGGGGCA GATGTCTCCC CTGCCACTCC TCAAACTCGC AGCAGTAATT TGTGGCACTA	2166
TGACAGCTAT TTTTATGACT ATCCTGTTCT GTGGGGGGGG GGTCTATGTT TTCCCCCAT	2226
ATTTGTATTC CTTTTCATAA CTTTCTTGA TATCTTTCCT CCCTCTTTTT TAATGTAAAG	2286
GTTTTCTCAA AAATTCTCCT AAAGGTGAGG GTCTCTTCT TTTCTTTTTT CCTTTTTTTT	2346
TTCTTTTTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGCG ATTATAGCCC	2406
GGTGCAGCCT CTAACCTCTG GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCG	2466
GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCCC	2526
CAGAGACACG GTCCCACCAT GTTACCCAGC CTGGTCTCAA ACTCCCAGC TAAAGCAGTC	2586
CTCCAGCCTC GGCTCCCAA AGTACTGGA TTACAGGCGT GAGCCCCAC GCTGGCCTGC	2646
TTTACGTATT TTCTTTTGTG CCCCTGCTCA CAGTGTTTTA GAGATGGCTT TCCCAGTGTG	2706
TGTTCAATTGT AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA	2766
AGTTGCTAGG AACATGTGGT GGGACTTTCA TATTCTGAAA AATGTTCTAT ATTCTCATTT	2826
TTCTAAAAGA AAGAAAAAG GAAACCCGAT TTATTTCTCC TGAATCTTTT TAAGTTTGTG	2886
TCGTTCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAATTTAT	2946
CCATGCTGGC AGAGGCACTC AGGTACTTGG TAAGCAAATT TCTAAACTC CAAGTTGCTG	3006
CAGCTTGGCA TTCTTCTTAT TCTAGAGGTC TCTCTGAAA AGATGGAGAA AATGAACAGG	3066
ACATGGGGCT CCTGGAAAGA AAGGGCCCGG GAAGTTCAAG GAAGAATAAA GTTGAAATTT	3126
TAAAAAAA	3136

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Pro	Leu	Phe	Ala	Leu	Leu	Leu
1				5					10					15	
Leu	Cys	Ala	Leu	Leu	Ala	Arg	Leu	Gln	Val	Ala	Leu	Gln	Ile	Ala	Pro
			20					25					30		
Pro	Cys	Thr	Ser	Glu	Lys	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	Asn
		35					40					45			

Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
 50 55 60  
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
 65 70 75 80  
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
 85 90 95  
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
 100 105 110  
 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
 115 120 125  
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
 130 135 140  
 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
 145 150 155 160  
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
 165 170 175  
 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
 180 185 190  
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
 195 200 205  
 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala  
 210 215 220  
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
 225 230 235 240  
 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg  
 245 250 255  
 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His  
 260 265 270  
 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu  
 275 280 285  
 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln  
 290 295 300  
 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln  
 305 310 315 320  
 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu  
 325 330 335  
 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg  
 340 345 350  
 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser  
 355 360 365  
 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp  
 370 375 380  
 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu  
 385 390 395 400  
 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met  
 405 410 415

Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro  
 420 425 430  
 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly  
 435 440 445  
 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro  
 450 455 460  
 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro  
 465 470 475 480  
 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly  
 485 490 495  
 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly  
 500 505 510  
 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn  
 515 520 525  
 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly  
 530 535 540  
 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala  
 545 550 555 560  
 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala  
 565 570 575  
 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys  
 580 585 590  
 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val  
 595 600 605  
 Gln Glu Gln Gly Gly Ala Lys Ala  
 610 615

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: FLAG® peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc mutein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
 1 5 10 15  
 Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
 20 25 30  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 35 40 45  
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 50 55 60  
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 65 70 75 80  
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 85 90 95  
 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 100 105 110  
 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
 115 120 125  
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
 130 135 140  
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg  
 145 150 155 160  
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
 165 170 175  
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 180 185 190  
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 195 200 205  
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 210 215 220  
 Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: CMV (R2780 Leader)



## (ix) FEATURE:

(D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide; Arg29 strengthens the furin cleavage site; nucleotides encoding Thr30 and Ser31 add a SpeI site.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr
1           5           10           15

Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser
          20           25           30

```

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1630 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY:  
 (B) CLONE: RANKL

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 3..884

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

CC GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG      47
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro
1           5           10           15

GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC      95
Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu
          20           25           30

CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG     143
Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu
          35           40           45

TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT     191
Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr
          50           55           60

CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GAT TTG CAG     239
His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln
          65           70           75

GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG     287
Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg
          80           85           90           95

ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT     335
Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile
          100           105           110

```

GTG	GGG	CCA	CAG	CGC	TTC	TCA	GGA	GCT	CCA	GCT	ATG	ATG	GAA	GGC	TCA	383
Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	
			115					120					125			
TGG	TTG	GAT	GTG	GCC	CAG	CGA	GGC	AAG	CCT	GAG	GCC	CAG	CCA	TTT	GCA	431
Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	
		130					135					140				
CAC	CTC	ACC	ATC	AAT	GCT	GCC	AGC	ATC	CCA	TCG	GGT	TCC	CAT	AAA	GTC	479
His	Leu	Thr	Ile	Asn	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val		
	145				150					155						
ACT	CTG	TCC	TCT	TGG	TAC	CAC	GAT	CGA	GGC	TGG	GCC	AAG	ATC	TCT	AAC	527
Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	
160				165					170						175	
ATG	ACG	TTA	AGC	AAC	GGA	AAA	CTA	AGG	GTT	AAC	CAA	GAT	GGC	TTC	TAT	575
Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	
			180					185						190		
TAC	CTG	TAC	GCC	AAC	ATT	TGC	TTT	CGG	CAT	CAT	GAA	ACA	TCG	GGA	AGC	623
Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	
			195					200					205			
GTA	CCT	ACA	GAC	TAT	CTT	CAG	CTG	ATG	GTG	TAT	GTC	GTT	AAA	ACC	AGC	671
Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	
		210				215					220					
ATC	AAA	ATC	CCA	AGT	TCT	CAT	AAC	CTG	ATG	AAA	GGA	GGG	AGC	ACG	AAA	719
Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	
	225					230					235					
AAC	TGG	TCG	GGC	AAT	TCT	GAA	TTC	CAC	TTT	TAT	TCC	ATA	AAT	GTT	GGG	767
Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	
240				245					250						255	
GGA	TTT	TTC	AAG	CTC	CGA	GCT	GGT	GAA	GAA	ATT	AGC	ATT	CAG	GTG	TCC	815
Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile	Ser	Ile	Gln	Val	Ser	
			260					265						270		
AAC	CCT	TCC	CTG	CTG	GAT	CCG	GAT	CAA	GAT	GCG	ACG	TAC	TTT	GGG	GCT	863
Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	
			275					280					285			
TTC	AAA	GTT	CAG	GAC	ATA	GAC	TGAGACTCAT	TTCGTGGAAC	ATTAGCATGG							914
Phe	Lys	Val	Gln	Asp	Ile	Asp										
		290														
ATGTCCTAGA	TGTTTTGAAA	CTTCTTAAAA	AATGGATGAT	GTCTATACAT	GTGTAAGACT											974
ACTAAGAGAC	ATGGCCACG	GTGTATGAAA	CTCACAGCCC	TCTCTCTTGA	GCCTGTACAG											1034
GTTGTGTATA	TGTAAAGTCC	ATAGGTGATG	TTAGATTTCAT	GGTGATTACA	CAACGGTTTT											1094
ACAATTTTGT	AATGATTTCC	TAGAATTGAA	CCAGATTGGG	AGAGGTATTC	CGATGCTTAT											1154
GAAAACTTA	CACGTGAGCT	ATGGAAGGGG	GTCACAGTCT	CTGGGTCTAA	CCCCTGGACA											1214
TGTGCCACTG	AGAACCTTGA	AATTAAGAGG	ATGCCATGTC	ATTGCAAAGA	AATGATAGTG											1274
TGAAGGGTTA	AGTTCTTTTG	AATTGTTACA	TTGCGCTGGG	ACCTGCAAAT	AAGTTCTTTT											1334
TTTCTAATGA	GGAGAGAAAA	ATATATGTAT	TTTTATATAA	TGCTAAAGT	TATATTTTCA											1394
GTGTAATGTT	TTCTGTGCAA	AGTTTTGTAA	ATTATATTTG	TGCTATAGTA	TTTGATTCAA											1454
AATATTTAAA	AATGTCTCAC	TGTTGACATA	TTTAATGTTT	TAAATGTACA	GATGTATTTA											1514
ACTGGTGCAC	TTTGTAATTC	CCCTGAAGGT	ACTCGTAGCT	AAGGGGGCAG	AATACTGTTT											1574

CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAAC TTAATAGAGT CTTCAG

1630

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala  
 1 5 10 15  
 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu  
 20 25 30  
 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr  
 35 40 45  
 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His  
 50 55 60  
 Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp  
 65 70 75 80  
 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met  
 85 90 95  
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val  
 100 105 110  
 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp  
 115 120 125  
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His  
 130 135 140  
 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr  
 145 150 155 160  
 Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met  
 165 170 175  
 Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr  
 180 185 190  
 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val  
 195 200 205  
 Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile  
 210 215 220  
 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn  
 225 230 235 240  
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 245 250 255  
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 260 265 270  
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 275 280 285  
 Lys Val Gln Asp Ile Asp  
 290

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY:  
 (B) CLONE: huRANKL (full length)
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..951
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	CGC	CGC	GCC	AGC	AGA	GAC	TAC	ACC	AAG	TAC	CTG	CGT	GGC	TCG	GAG	48
Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	
1				5					10					15		
GAG	ATG	GGC	GGC	GGC	CCC	GGA	GCC	CCG	CAC	GAG	GGC	CCC	CTG	CAC	GCC	96
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala	
		20						25					30			
CCG	CCG	CCG	CCT	GCG	CCG	CAC	CAG	CCC	CCC	GCC	GCC	TCC	CGC	TCC	ATG	144
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	
		35					40					45				
TTC	GTG	GCC	CTC	CTG	GGG	CTG	GGG	CTG	GGC	CAG	GTT	GTC	TGC	AGC	GTC	192
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	
	50				55						60					
GCC	CTG	TTC	TTC	TAT	TTC	AGA	GCG	CAG	ATG	GAT	CCT	AAT	AGA	ATA	TCA	240
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	
65				70					75					80		
GAA	GAT	GGC	ACT	CAC	TGC	ATT	TAT	AGA	ATT	TTG	AGA	CTC	CAT	GAA	AAT	288
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	
			85						90					95		
GCA	GAT	TTT	CAA	GAC	ACA	ACT	CTG	GAG	AGT	CAA	GAT	ACA	AAA	TTA	ATA	336
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	
		100						105					110			
CCT	GAT	TCA	TGT	AGG	AGA	ATT	AAA	CAG	GCC	TTT	CAA	GGA	GCT	GTG	CAA	384
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	
		115					120					125				
AAG	GAA	TTA	CAA	CAT	ATC	GTT	GGA	TCA	CAG	CAC	ATC	AGA	GCA	GAG	AAA	432
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	
	130				135						140					
GCG	ATG	GTG	GAT	GGC	TCA	TGG	TTA	GAT	CTG	GCC	AAG	AGG	AGC	AAG	CTT	480
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	
145					150					155					160	

GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC CCA	528
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	
165 170 175	
TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG GGT	576
Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly	
180 185 190	
TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA GTT	624
Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val	
195 200 205	
AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA CAT	672
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
210 215 220	
CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG GTG	720
His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val	
225 230 235 240	
TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG ATG	768
Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met	
245 250 255	
AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT TTT	816
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe	
260 265 270	
TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG GAA	864
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu	
275 280 285	
ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG GAT	912
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
290 295 300	
GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT TGA	954
Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp	
305 310 315	

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu	
1 5 10 15	
Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala	
20 25 30	
Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met	
35 40 45	
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val	
50 55 60	
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser	
65 70 75 80	
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	
85 90 95	

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
 100 105 110  
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
 115 120 125  
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
 130 135 140  
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
 145 150 155 160  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
 165 170 175  
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
 180 185 190  
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 195 200 205  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 210 215 220  
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 225 230 235 240  
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 245 250 255  
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 260 265 270  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 275 280 285  
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 290 295 300  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1878 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Murine
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Murine Fetal Liver Epithelium
  - (B) CLONE: muRANK
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1875

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	GCC	CCG	CGC	GCC	CGG	CGG	CGC	CGC	CAG	CTG	CCC	GCG	CCG	CTG	CTG	48
Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Gln	Leu	Pro	Ala	Pro	Leu	Leu	
1				5					10					15		
GCG	CTC	TGC	GTG	CTG	CTC	GTT	CCA	CTG	CAG	GTG	ACT	CTC	CAG	GTC	ACT	96
Ala	Leu	Cys	Val	Leu	Leu	Val	Pro	Leu	Gln	Val	Thr	Leu	Gln	Val	Thr	
			20					25					30			
CCT	CCA	TGC	ACC	CAG	GAG	AGG	CAT	TAT	GAG	CAT	CTC	GGA	CGG	TGT	TGC	144
Pro	Pro	Cys	Thr	Gln	Glu	Arg	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	
		35					40					45				
AGC	AGA	TGC	GAA	CCA	GGA	AAG	TAC	CTG	TCC	TCT	AAG	TGC	ACT	CCT	ACC	192
Ser	Arg	Cys	Glu	Pro	Gly	Lys	Tyr	Leu	Ser	Ser	Lys	Cys	Thr	Pro	Thr	
	50					55					60					
TCC	GAC	AGT	GTG	TGT	CTG	CCC	TGT	GGC	CCC	GAT	GAG	TAC	TTG	GAC	ACC	240
Ser	Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Thr	
65				70						75					80	
TGG	AAT	GAA	GAA	GAT	AAA	TGC	TTG	CTG	CAT	AAA	GTC	TGT	GAT	GCA	GGC	288
Trp	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Ala	Gly	
				85					90					95		
AAG	GCC	CTG	GTG	GCG	GTG	GAT	CCT	GGC	AAC	CAC	ACG	GCC	CCG	CGT	CGC	336
Lys	Ala	Leu	Val	Ala	Val	Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg	
			100					105					110			
TGT	GCT	TGC	ACG	GCT	GGC	TAC	CAC	TGG	AAC	TCA	GAC	TGC	GAG	TGC	TGC	384
Cys	Ala	Cys	Thr	Ala	Gly	Tyr	His	Trp	Asn	Ser	Asp	Cys	Glu	Cys	Cys	
		115					120					125				
CGC	AGG	AAC	ACG	GAG	TGT	GCA	CCT	GGC	TTC	GGA	GCT	CAG	CAT	CCC	TTG	432
Arg	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu	
	130					135					140					
CAG	CTC	AAC	AAG	GAT	ACG	GTG	TGC	ACA	CCC	TGC	CTC	CTG	GGC	TTC	TTC	480
Gln	Leu	Asn	Lys	Asp	Thr	Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe	
145				150					155					160		
TCA	GAT	GTC	TTT	TCG	TCC	ACA	GAC	AAA	TGC	AAA	CCT	TGG	ACC	AAC	TGC	528
Ser	Asp	Val	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys	
				165				170					175			
ACC	CTC	CTT	GGA	AAG	CTA	GAA	GCA	CAC	CAG	GGG	ACA	ACG	GAA	TCA	GAT	576
Thr	Leu	Leu	Gly	Lys	Leu	Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp	
			180					185					190			
GTG	GTC	TGC	AGC	TCT	TCC	ATG	ACA	CTG	AGG	AGA	CCA	CCC	AAG	GAG	GCC	624
Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	
		195					200					205				
CAG	GCT	TAC	CTG	CCC	AGT	CTC	ATC	GTT	CTG	CTC	CTC	TTC	ATC	TCT	GTG	672
Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	
	210					215					220					
GTA	GTA	GTG	GCT	GCC	ATC	ATC	TTC	GGC	GTT	TAC	TAC	AGG	AAG	GGA	GGG	720
Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	
225					230				235					240		
AAA	GCG	CTG	ACA	GCT	AAT	TTG	TGG	AAT	TGG	GTC	AAT	GAT	GCT	TGC	AGT	768
Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	
				245				250					255			
AGT	CTA	AGT	GGA	AAT	AAG	GAG	TCC	TCA	GGG	GAC	CGT	TGT	GCT	GGT	TCC	816
Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	
			260				265						270			

CAC	TCG	GCA	ACC	TCC	AGT	CAG	CAA	GAA	GTG	TGT	GAA	GGT	ATC	TTA	CTA	864
His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	
		275					280					285				
ATG	ACT	CGG	GAG	GAG	AAG	ATG	GTT	CCA	GAA	GAC	GGT	GCT	GGA	GTC	TGT	912
Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	
	290					295					300					
GGG	CCT	GTG	TGT	GCG	GCA	GGT	GGG	CCC	TGG	GCA	GAA	GTC	AGA	GAT	TCT	960
Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	
305					310					315					320	
AGG	ACG	TTC	ACA	CTG	GTC	AGC	GAG	GTT	GAG	ACG	CAA	GGA	GAC	CTC	TCG	1008
Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	
				325					330					335		
AGG	AAG	ATT	CCC	ACA	GAG	GAT	GAG	TAC	ACG	GAC	CGG	CCC	TCG	CAG	CCT	1056
Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Pro	Gln	Pro	
			340					345					350			
TCG	ACT	GGT	TCA	CTG	CTC	CTA	ATC	CAG	CAG	GGA	AGC	AAA	TCT	ATA	CCC	1104
Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	
		355					360					365				
CCA	TTC	CAG	GAG	CCC	CTG	GAA	GTG	GGG	GAG	AAC	GAC	AGT	TTA	AGC	CAG	1152
Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	
	370					375					380					
TGT	TTC	ACC	GGG	ACT	GAA	AGC	ACG	GTG	GAT	TCT	GAG	GGC	TGT	GAC	TTC	1200
Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	
385					390					395					400	
ACT	GAG	CCT	CCG	AGC	AGA	ACT	GAC	TCT	ATG	CCC	GTG	TCC	CCT	GAA	AAG	1248
Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	
				405					410					415		
CAC	CTG	ACA	AAA	GAA	ATA	GAA	GGT	GAC	AGT	TGC	CTC	CCC	TGG	GTG	GTC	1296
His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	
			420					425					430			
AGC	TCC	AAC	TCA	ACA	GAT	GGC	TAC	ACA	GGC	AGT	GGG	AAC	ACT	CCT	GGG	1344
Ser	Ser	Asn	Ser	Thr	Asp	Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	
		435					440					445				
GAG	GAC	CAT	GAA	CCC	TTT	CCA	GGG	TCC	CTG	AAA	TGT	GGA	CCA	TTG	CCC	1392
Glu	Asp	His	Glu	Pro	Phe	Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	
	450					455					460					
CAG	TGT	GCC	TAC	AGC	ATG	GGC	TTT	CCC	AGT	GAA	GCA	GCA	GCC	AGC	ATG	1440
Gln	Cys	Ala	Tyr	Ser	Met	Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	
465					470					475					480	
GCA	GAG	GCG	GGA	GTA	CGG	CCC	CAG	GAC	AGG	GCT	GAT	GAG	AGG	GGA	GCC	1488
Ala	Glu	Ala	Gly	Val	Arg	Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	
				485					490					495		
TCA	GGG	TCC	GGG	AGC	TCC	CCC	AGT	GAC	CAG	CCA	CCT	GCC	TCT	GGG	AAC	1536
Ser	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	
			500					505					510			
GTG	ACT	GGA	AAC	AGT	AAC	TCC	ACG	TTC	ATC	TCT	AGC	GGG	CAG	GTG	ATG	1584
Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	
		515					520					525				
AAC	TTC	AAG	GGT	GAC	ATC	ATC	GTG	GTG	TAT	GTC	AGC	CAG	ACC	TCG	CAG	1632
Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	
	530					535					540					
GAG	GGC	CCG	GGT	TCC	GCA	GAG	CCC	GAG	TCG	GAG	CCC	GTG	GGC	CGC	CCT	1680



Glu 545	Gly	Pro	Gly	Ser	Ala 550	Glu	Pro	Glu	Ser	Glu 555	Pro	Val	Gly	Arg	Pro 560	
GTG	CAG	GAG	GAG	ACG	CTG	GCA	CAC	AGA	GAC	TCC	TTT	GCG	GGC	ACC	GCG	1728
Val	Gln	Glu	Glu	Thr 565	Leu	Ala	His	Arg	Asp 570	Ser	Phe	Ala	Gly	Thr 575	Ala	
CCG	CGC	TTC	CCC	GAC	GTC	TGT	GCC	ACC	GGG	GCT	GGG	CTG	CAG	GAG	CAG	1776
Pro	Arg	Phe	Pro 580	Asp	Val	Cys	Ala	Thr 585	Gly	Ala	Gly	Leu	Gln 590	Glu	Gln	
GGG	GCA	CCC	CGG	CAG	AAG	GAC	GGG	ACA	TCG	CGG	CCG	GTG	CAG	GAG	CAG	1824
Gly	Ala	Pro 595	Arg	Gln	Lys	Asp	Gly 600	Thr	Ser	Arg	Pro	Val 605	Gln	Glu	Gln	
GGT	GGG	GCG	CAG	ACT	TCA	CTC	CAT	ACC	CAG	GGG	TCC	GGA	CAA	TGT	GCA	1872
Gly	Gly	Ala	Gln	Thr	Ser	Leu	His	Thr	Gln	Gly	Ser	Gly	Gln	Cys	Ala	
610						615				620						
GAA	TGA															1878
Glu 625																

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Gln	Leu	Pro	Ala	Pro	Leu	Leu
1				5					10					15	
Ala	Leu	Cys	Val	Leu	Leu	Val	Pro	Leu	Gln	Val	Thr	Leu	Gln	Val	Thr
			20					25					30		
Pro	Pro	Cys	Thr	Gln	Glu	Arg	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys
		35					40					45			
Ser	Arg	Cys	Glu	Pro	Gly	Lys	Tyr	Leu	Ser	Ser	Lys	Cys	Thr	Pro	Thr
50						55					60				
Ser	Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Thr
65					70					75				80	
Trp	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Ala	Gly
				85					90					95	
Lys	Ala	Leu	Val	Ala	Val	Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg
			100					105					110		
Cys	Ala	Cys	Thr	Ala	Gly	Tyr	His	Trp	Asn	Ser	Asp	Cys	Glu	Cys	Cys
		115					120					125			
Arg	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu
130						135					140				
Gln	Leu	Asn	Lys	Asp	Thr	Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe
145					150					155					160
Ser	Asp	Val	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys
				165					170					175	
Thr	Leu	Leu	Gly	Lys	Leu	Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp
			180					185					190		

Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala		
		195					200					205					
Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val		
	210					215					220						
Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly		
225					230					235					240		
Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser		
				245					250					255			
Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser		
			260					265					270				
His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu		
		275					280					285					
Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys		
	290					295					300						
Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser		
305					310					315					320		
Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser		
				325					330					335			
Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro		
			340					345						350			
Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro		
		355					360					365					
Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln		
	370					375					380						
Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe		
385					390					395					400		
Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys		
				405					410					415			
His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val		
			420					425					430				
Ser	Ser	Asn	Ser	Thr	Asp	Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly		
		435					440					445					
Glu	Asp	His	Glu	Pro	Phe	Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro		
	450					455					460						
Gln	Cys	Ala	Tyr	Ser	Met	Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met		
465					470					475					480		
Ala	Glu	Ala	Gly	Val	Arg	Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala		
				485					490					495			
Ser	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn		
			500					505					510				
Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met		
		515					520					525					
Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln		
	530					535					540						
Glu	Gly	Pro	Gly	Ser	Ala	Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro		
545					550					555					560		

(2) INFORMATION FOR SEQ ID NO:16:

(ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:17:

(ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:18:

(ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:19:

62

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile  
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu  
20 25 30

Arg